Fig. 4A and 4B:	Nucleic acid sequence (SEQ ID No. 1) and deduced protein sequence (SEQ ID No. 2) of monkey SR-p70a.
Fig. 5:	Partial nucleic acid sequence (SEQ ID No. 3) and complete deduced protein sequence (SEQ ID No. 4) of monkey SR-p70b.
Fig. 6A and 6B:	Partial nucleic acid sequence (SEQ ID No. 5) and deduced complete protein sequence (SEQ ID No. 6) of human SR-p70a.
Fig. 7:	Partial nucleic acid sequence (SEQ ID No. 7) and complete deduced protein sequence (SEQ ID No. 8) of mouse SR-p70c.
Fig. 8:	Partial nucleic acid sequence (SEQ ID No. 9) and partially deduced protein sequence (SEQ ID No. 10) of mouse SR-p70a.
Fig. 9A and 9B:	Multialignment of the proteins deduced from monkey (SR-p70a-cos3 and SR-p70b-cos3) (SEQ ID No. 2 and SEQ ID No. 4, respectively), human (SR-p70-ht29) and mouse (SR-p70c-att20 and sr-p70a-att20) (SEQ ID No. 10 and SEQ ID No. 8, respectively) SR-p70 cDNAs.
Fig. 10a:	Immunoblot of the SR-p70 protein.
Fig. 10b:	Detection of the endogenous SR-p70 protein.
Fig. 11:	Chromosomal localization of the human SR-p70 gene. The signal appears on chromosome 1, in the p36 region.
Fig. 12:	Genomic structure of the SR-p70 gene and comparison with that of the p53 gene. The human protein sequences of SR-p70a (SEQ ID No. 6) (upper line of the alignment) and of p53 (SEQ ID No. 45) (lower line) are divided up into peptides on the basis of the respective exons from which they are encoded. The figures beside the arrows correspond to the numbering of the corresponding exons.
Fig. 13:	Human genomic sequence of SR-p70 from the 3' end of intron 1 to the 5' end of exon 3 (SEQ ID No. 46). The introns are boxed. At positions 123 and 133, two variable nucleic acid positions are localized (G → A at 123 and C → T at 133). The restriction sites for the enzyme StyI are underlined (position 130 in the case where a T is present instead of a C at position 133, position 542 and position 610). The arrows indicate the positions of the nucleic acid primers used in Example XI.

B' Cont'

Fig. 14: Nucleic acid comparison of the 5' region of the human cDNAs of SR-p70d (SEQ ID No. 12) and of SR-p70a (SEQ ID No. 5).

Fig. 15A-J: Multialignment of the nucleic acid sequences corresponding to human SR-p70a, b, d, e, and f (SEQ ID No. 5, SEQ ID No. 18, SEQ ID No. 12, SEQ ID No. 14 and SEQ ID No. 16, respectively).

Fig. 16A-C: Multialignment of the proteins deduced from human SR-p70 (a, b, d, e and f) (SEQ ID No. 6, SEQ ID No. 19, SEQ ID No. 13, SEQ ID No. 15 and SEQ ID No. 17, respectively), cDNA's.

Fig. 17: Partial nucleic acid sequence (SEQ ID No. 5) and partial deduced protein sequence (SEQ ID No. 6) of human SR-p70a. The two bases in bold characters correspond to two variable positions (see Figure 6). This sequence possesses a more complete non-coding 5' region than the one presented in Figure 6.

Fig. 18: Analysis of the SR-p70a transcripts after PCR amplification.
lane M: 1 kb ladder (GIBCO-BRL) molecular weight markers
lane 1: line HT29
lane 3: line SK-N-AS
lane 5: line UMR-32
lane 7: line U-373 MG
lane 9: line SW 480
lane 11: line CHP 212
lane 13: line SK-N-MC

B1 Cont

lanes 2, 4, 6, 8, 10, 12, 14: negative controls corresponding to lanes 1, 3, 5, 7, 9, 11 and 13, respectively (absence of inverse transcriptase in the RT-PCR reaction).

Fig. 19A and 19B:

A: Analysis by agarose gel electrophoresis of genomic fragments amplified by PCR (from the 3' end of intron 1 to the 5' end of exon 3). The numbering of the lanes corresponds to the numbering of the control population. Lane M: molecular weight markers (1 kb ladder).

B: Analysis identical to that of part A, after digestion of the same samples with the restriction enzyme StyI.

B1 Cont

Fig. 20: Diagrammatic representation with a partial restriction map of the plasmid pCDNA3 containing human SR-p70a.

Corresponding amendments have made in the drawings as shown in red on the copies submitted herewith pursuant to 37 CFR 1.121(d).

In the Claims

Please amend Claims 1, 4 and 33 to read as follows:

1.(Twice Amended) A purified polypeptide, comprising an amino acid sequence selected from the group consisting of:

a) sequence SEQ ID No. 2;

b) sequence SEQ ID No. 4;

c) sequence SEQ ID No. 6;

d) sequence SEQ ID No. 8;

e) sequence SEQ ID No. 10;

f) sequence SEQ ID No. 13;

g) sequence SEQ ID No. 15;

h) sequence SEQ ID No. 17;

i) sequence SEQ ID No. 19; and

j) any sequence derived from SEQ ID No. 2, SEQ ID No. 4, SEQ ID No. 6, SEQ ID No. 8, SEQ ID No. 10, SEQ ID No. 13, SEQ ID No. 15, SEQ ID No. 17 or SEQ ID No. 19 and having substantially the same biological activity.

B2 and C1

4. (Twice Amended) A polypeptide according to Claim 1, which is produced from an alternative splicing of messenger RNA of a gene coding for said polypeptide.

B3

33. (Twice Amended) A pharmaceutical composition for the treatment of pathologies linked to apoptosis or cell transformation comprising an effective amount of the polypeptide according to Claim 1.

B4